

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Conley, Pamela B.
Jantzen, Hans-Michael
- (ii) TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
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 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20036-5869
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/749,707
 - (B) FILING DATE: 15-NOV-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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 - (C) REFERENCE/DOCKET NUMBER: 044481-5010-01-US
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 625..1626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATAAAGTATG TTTAGCCCTC ATGTCACATG AACCTTTATG CATTGAAGAT TGTTTCCCTT

60

CCCCCCCCAG GGGGTGGGGT TATTTTCTA TCCTTGTTAA CTCCCTATA TTATTATATA	120
CACTTTGAGT TTTAGGGTAC ATGTGCACAA AGTGCAGGTT AGTTACATAT GTATACATGT	130
GCCAIGTTGG TGTGCTGCAC CCATTAACAC ATCATTTAGC ATGAGGTATA TCTCCTAATG	240
TTATCCCTCC CCCCTCCCCC CACCCACAA CAGTCCCCGG AGTGTGATAT TCCCCTTTCC	300
TGTGTCCATG TGTATTATT CCAATTCCCC ACCTATGAAG TGAAAATATG CAGGTGTTTG	360
GATTTTGTG CTTGGCAATA GTTTTGCTGA GAATGATGGT TTCCAGCTTC ATCCATGTCC	420
CTACAAAGGA CATGAACCTA TCATTTTTTA TGACTGCATA GTATTCTATG GTGTATACAT	480
GCCAACTTTT CCCCCCCCCC TTTTAAAGCT CCTTCTTTCA CTGGCTTTCA TGATCCCACC	540
AATTCTGCT TTTCTTTTTT TGTTTTTTTC TTCCAACAGA ATGGTTATGG ITTAACTCAG	600
CAGAATTTGT TGAACAACTA CGAC ATG CTG GGG ATC ATG GCA TGG AAT GCA	651
Met Leu Gly Ile Met Ala Trp Asn Ala	
1 5	
ACT TGC AAA AAC TGG CTG GCA GCA GAG GCT GCC CTG GAA AAG TAC TAC	699
Thr Cys Lys Asn Trp Leu Ala Ala Glu Ala Ala Leu Glu Lys Tyr Tyr	
10 15 20 25	
CTT TCC ATT TTT TAT GGG ATT GAG TTC GTT GTG GGA GTC CTT GGA AAT	747
Leu Ser Ile Phe Tyr Gly Ile Glu Phe Val Val Gly Val Leu Gly Asn	
30 35 40	
ACC ATT GTT GTT TAC GGC TAC ATC TTC TCT CTG AAG AAC TGG AAC AGC	795
Thr Ile Val Val Tyr Gly Tyr Ile Phe Ser Leu Lys Asn Trp Asn Ser	
45 50 55	
AGT AAT ATT TAT CTC TTT AAC CTC TCT GTC TCT GAC TTA GCT TTT CTG	843
Ser Asn Ile Tyr Leu Phe Asn Leu Ser Val Ser Asp Leu Ala Phe Leu	
60 65 70	
TGC ACC CTC CCC ATG CTG ATA AGG AGT TAT GCC AAT GGA AAC TGG ATA	891
Cys Thr Leu Pro Met Leu Ile Arg Ser Tyr Ala Asn Gly Asn Trp Ile	
75 80 85	
TAT GGA GAC GTG CTC TGC ATA AGC AAC CGA TAT GTG CTT CAT GCC AAC	939
Tyr Gly Asp Val Leu Cys Ile Ser Asn Arg Tyr Val Leu His Ala Asn	
90 95 100 105	
CTC TAT ACC AGC ATT CTC TTT CTC ACT TTT ATC AGC ATA GAT CGA TAC	987
Leu Tyr Thr Ser Ile Leu Phe Leu Thr Phe Ile Ser Ile Asp Arg Tyr	
110 115 120	
TTG ATA ATT AAG TAT CCT TTC CGA GAA CAC CTT CTG CAA AAG AAA GAG	1035
Leu Ile Ile Lys Tyr Pro Phe Arg Glu His Leu Leu Gln Lys Lys Glu	
125 130 135	
TTT GCT ATT TTA ATC TCC TTG GCC ATT TGG GTT TTA GTA ACC TTA GAG	1083
Phe Ala Ile Leu Ile Ser Leu Ala Ile Trp Val Leu Val Thr Leu Glu	
140 145 150	
TTA CTA CCC ATA CTT CCC CTT ATA AAT CCT GTT ATA ACT GAC AAT GGC	1131
Leu Leu Pro Ile Leu Pro Leu Ile Asn Pro Val Ile Thr Asp Asn Gly	
155 160 165	

ACC ACC TGT AAT GAT TTT GCA AGT TCT GGA GAC CCC AAC TAC AAC CTC Thr Thr Cys Asn Asp Phe Ala Ser Ser Gly Asp Pro Asn Tyr Asn Leu 170 175 180 185	1179
ATT TAC AGC ATG TGT CTA ACA CTG TTG GGG TTC CTT ATT CCT CTT TTT Ile Tyr Ser Met Cys Leu Thr Leu Leu Gly Phe Leu Ile Pro Leu Phe 190 195 200	1227
GTG ATG TGT TTC TTT TAT TAC AAG ATT GCT CTC TTC CTA AAG CAG AGG Val Met Cys Phe Phe Tyr Tyr Lys Ile Ala Leu Phe Leu Lys Gln Arg 205 210 215	1275
AAT AGG CAG GTT GCT ACT GCT CTG CCC CTT GAA AAG CCT CTC AAC TTG Asn Arg Gln Val Ala Thr Ala Leu Pro Leu Glu Lys Pro Leu Asn Leu 220 225 230	1323
GTC ATC ATG GCA GTG GTA ATC TTC TCT GTG CTT TTT ACA CCC TAT CAC Val Ile Met Ala Val Val Ile Phe Ser Val Leu Phe Thr Pro Tyr His 235 240 245	1371
GTC ATG CGG AAT GTG AGG ATC GCT TCA CGC CTG GGG AGT TGG AAG CAG Val Met Arg Asn Val Arg Ile Ala Ser Arg Leu Gly Ser Trp Lys Gln 250 255 260 265	1419
TAT CAG TGC ACT CAG GTC GTC ATC AAC TCC TTT TAC ATT GTG ACA CGG Tyr Gln Cys Thr Gln Val Val Ile Asn Ser Phe Tyr Ile Val Thr Arg 270 275 290	1467
GCT TTG GGC TTT CTG AAC AGT GTC ATC AAC CCT GTC TTC TAT TTT CTT Ala Leu Gly Phe Leu Asn Ser Val Ile Asn Pro Val Phe Tyr Phe Leu 285 290 295	1515
TTG GGA GAT CAC TTC AGG GAC ATG CTG ATG AAT CAA CTG AGA CAC AAC Leu Gly Asp His Phe Arg Asp Met Leu Met Asn Gln Leu Arg His Asn 300 305 310	1563
TTC AAA TCC CTT ACA TCC TTT AGC AGA TGG GCT CAT GAA CTC CTA CTT Phe Lys Ser Leu Thr Ser Phe Ser Arg Trp Ala His Glu Leu Leu Leu 315 320 325	1611
TCA TTC AGA GAA AAG TGAGGGGCTT GTGAAACAGA TTGTTCTACA GATGAATCTG Ser Phe Arg Glu Lys 330	1666
TAAGCCAGTT ACAGTTTGCT TTAACTCATA GACATCAATC AGAGAGTGTC ACAGATTTAA	1725
CCTTGATCTA AAGACAAGTT GTACCCAGAG TATGTGAAAA GAATGGGACG ACAAGAATGT	1786
ACTGGTTTCT TCCTCTAAGA ATTGAAAGGA GTTGAAGTGC CTTATGTTTG GGCATGTAAC	1846
TCCAAAATAC TAGGTAGTAT AAGGCTTTCT CAATCAGTCC CCAAATGGAA GATATATAAA	1905
GCAACAAGTT GTCTGCATTT GATCACTGGT CAGATTGTAA AAAAAAAAAA AAAAAAGGGC	1966
GCCCGCCACC GCGGTGGAGC TCCAATCGCC	1996

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
 1           5           10           15
Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
      20           25           30
Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
      35           40           45
Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
      50           55           60
Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
      65           70           75           90
Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
      85           90           95
Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
      100          105          110
Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
      115          120          125
Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
      130          135          140
Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
      145          150          155          160
Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
      165          170          175
Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
      180          185          190
Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
      195          200          205
Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
      210          215          220
Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
      225          230          235          240
Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
      245          250          255
Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
      260          265          270
Ile Asn Ser Phe Tyr Ile Val Thr Arg Ala Leu Gly Phe Leu Asn Ser
      275          280          285

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Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
 290 295 300
 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
 305 310 315 320
 Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Asp Leu Gly Pro Trp Asn Asp Thr Ile Asn Gly Thr Trp
 1 5 10 15
 Asp Gly Asp Glu Leu Gly Tyr Arg Cys Arg Phe Asn Glu Asp Phe Lys
 20 25 30
 Tyr Val Leu Leu Pro Val Ser Tyr Gly Val Val Cys Val Leu Gly Leu
 35 40 45
 Cys Leu Asn Ala Val Gly Leu Tyr Ile Phe Leu Cys Arg Leu Lys Thr
 50 55 60
 Trp Asn Ala Ser Thr Thr Tyr Met Phe His Leu Ala Val Ser Asp Ala
 65 70 75 80
 Leu Tyr Ala Ala Ser Leu Pro Leu Leu Val Tyr Tyr Tyr Ala Arg Gly
 85 90 95
 Asp His Trp Pro Phe Ser Thr Val Leu Cys Lys Leu Val Arg Phe Leu
 100 105 110
 Phe Tyr Thr Asn Leu Tyr Cys Ser Ile Leu Phe Leu Thr Cys Ile Ser
 115 120 125
 Val His Arg Cys Leu Gly Val Leu Arg Pro Leu Arg Ser Leu Arg Trp
 130 135 140
 Gly Arg Ala Arg Tyr Ala Arg Arg Val Ala Gly Ala Val Trp Val Leu
 145 150 155 160
 Val Leu Ala Cys Gln Ala Pro Val Leu Tyr Phe Val Thr Thr Ser Ala
 165 170 175
 Arg Gly Pro Leu Thr Cys His Asp Thr Ser Ala Pro Glu Leu Phe Ser
 180 185 190

Arg Phe Val Ala Tyr Ser Ser Val Met Leu Gly Leu Leu Phe Ala Val
 195 200 205
 Pro Phe Ala Val Ile Leu Val Cys Tyr Val Leu Met Ala Arg Arg Leu
 210 215 220
 Leu Lys Pro Ala Tyr Gly Thr Ser Gly Gly Leu Pro Arg Ala Lys Arg
 225 230 235 240
 Lys Ser Val Arg Thr Ile Ala Val Val Leu Ala Val Phe Ala Leu Cys
 245 250 255
 Phe Leu Pro Phe His Val Thr Arg Thr Leu Tyr Tyr Ser Phe Arg Ser
 260 265 270
 Leu Asp Leu Ser Cys His Thr Leu Asn Ala Ile Asn Met Ala Tyr Lys
 275 280 285
 Val Thr Arg Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val Leu Tyr
 290 295 300
 Phe Leu Ala Gly Gln Arg Leu Val Arg Phe Ala Arg Asp Ala Lys Pro
 305 310 315 320
 Pro Thr Gly Pro Ser Pro Ala Thr Pro Ala Arg Arg Thr Leu Gly Leu
 325 330 335
 Arg Arg Ser Asp Arg Thr Asp Met Gln Arg Ile Gly Asp Val Leu Gly
 340 345 350
 Ser Ser Glu Asp Ser Arg Arg Thr Glu Ser Thr Pro Ala Gly Ser Glu
 355 360 365
 Asn Thr Lys Asp Ile Arg Leu
 370 375

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Glu Val Leu Trp Pro Ala Val Pro Asn Gly Thr Asp Thr Ala
 1 5 10 15
 Phe Leu Ala Asp Pro Gly Ser Pro Trp Gly Asn Ser Thr Val Thr Ser
 20 25 30
 Thr Ala Ala Val Ala Ser Pro Phe Lys Cys Ala Leu Thr Lys Thr Gly
 35 40 45

Phe Gln Phe Tyr Tyr Leu Pro Ala Val Tyr Ile Leu Val Phe Ile Ile
 50 55 60
 Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met Phe Val Phe His Met
 65 70 75 80
 Lys Pro Trp Ser Gly Ile Ser Val Tyr Met Phe Asn Leu Ala Leu Ala
 85 90 95
 Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu Ile Phe Tyr Tyr Phe
 100 105 110
 Asn Lys Thr Asp Trp Ile Phe Gly Asp Ala Met Cys Lys Leu Gln Arg
 115 120 125
 Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile Leu Phe Leu Thr Cys
 130 135 140
 Ile Ser Ala His Arg Tyr Ser Gly Val Val Tyr Pro Leu Lys Ser Leu
 145 150 155 160
 Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Ile Ser Val Leu Val Trp
 165 170 175
 Leu Ile Val Val Val Gly Ile Ser Pro Ile Leu Phe Tyr Ser Gly Thr
 180 185 190
 Gly Ile Arg Lys Asn Lys Thr Ile Thr Cys Tyr Asp Thr Thr Ser Asp
 195 200 205
 Glu Tyr Leu Arg Ser Tyr Phe Ile Tyr Ser Met Cys Thr Thr Val Ala
 210 215 220
 Met Phe Cys Val Pro Leu Val Leu Ile Leu Gly Cys Tyr Gly Leu Ile
 225 230 235 240
 Val Arg Ala Leu Ile Tyr Lys Asp Leu Asp Asn Ser Pro Leu Arg Arg
 245 250 255
 Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr Val Phe Ala Val Ser
 260 265 270
 Tyr Ile Pro Phe His Val Met Lys Thr Met Asn Leu Arg Ala Arg Leu
 275 280 285
 Asp Phe Gln Thr Pro Glu Met Cys Ala Phe Asn Asp Arg Val Tyr Ala
 290 295 300
 Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu Asn Ser Cys Val Asp
 305 310 315 320
 Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe Arg Arg Arg Leu Ser
 325 330 335
 Arg Ala Thr Arg Lys Ala Ser Arg Arg Ser Glu Ala Asn Leu Gln Ser
 340 345 350
 Lys Ser Glu Asp Met Thr Leu Asn Ile Leu Ser Glu Phe Lys Gln Asn
 355 360 365

Gly Asp Thr Ser Leu
370

(2) INFORMATION FOR SEQ ID NO:5:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
1 5 10 15
Ala Glu Ala Ala Leu Glu Lys
 20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser
 1 5 10 15
 Ser Gly Asp Pro Asn Tyr
 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
 1 5 10 15
 Ile Asn Ser Phe
 20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATYCTBTTC TGACHTGYAT YWSNGTBCA

29

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

(2) INFORMATION FOR SEQ ID NO:12:

(ii) MOLECULE TYPE: peptide

Lys Glu Phe Ala Ile Leu
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Leu Pro Leu Glu Lys Pro Leu Asn Leu
20 25

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His	Phe	Arg	Asp	Met	Leu	Met	Asn	Gln	Leu	Arg	His	Asn	Phe	Lys	Ser
1				5					10					15	
Leu	Thr	Ser	Phe	Ser	Arg	Trp	Ala	His	Glu	Leu	Leu	Leu	Ser	Phe	Arg
			20					25					30		
Glu Lys															